

(b) determining and evaluating for each of said oligonucleotides at least one parameter that is predictive of the ability of each of said oligonucleotides to hybridize to said target nucleotide sequence,

(c) selecting a subset of oligonucleotides within said predetermined number of non-identical oligonucleotides based on an examination of said parameter,

(d) identifying oligonucleotides in said subset that are in clusters along a region of said nucleotide sequence that is hybridizable to said target nucleotide sequence and

(e) selecting, for a cluster, a hybridization oligonucleotide.

B1
3. (amended) A method according to Claim 1 wherein said non-identical oligonucleotides are of identical length N.

B2
4. (amended) A method according to Claim 3 wherein said non-identical oligonucleotides are spaced one nucleotide apart, said predetermined number comprising $L-N+1$ oligonucleotides, where L is the length of the hybridizable sequence.

B3
10. (amended) A method according to Claim 1 wherein said parameter is derived from a factor by mathematical transformation of said factor wherein said factor is predictive of the ability of an oligonucleotide to hybridize with a target nucleotide sequence.

B4
24. (amended) A method according to Claim 1 wherein step (c) comprises identifying a subset of oligonucleotides within said predetermined number of non-identical oligonucleotides by establishing cut-off values for said parameter.

25. (amended) A method according to Claim 1 wherein said step (c) comprises identifying a subset of oligonucleotides within said predetermined number of non-identical oligonucleotides by converting the values of said parameter into a dimensionless number.

B5
38. (amended) A method according to Claim 1 which comprises (i) identifying a subset of oligonucleotides within said predetermined number of non-identical

oligonucleotides by establishing cut-off values for each of said parameters.

98. **(twice amended)** A computer based method for selecting a hybridization oligonucleotide to hybridize to a target nucleotide sequence, said method comprising:

(a) identifying under computer control a predetermined number of non-identical oligonucleotides within a nucleotide sequence that is hybridizable with said target nucleotide sequence, said oligonucleotides being chosen to sample a length of said nucleotide sequence,

(b) under computer control, determining and evaluating for each of said oligonucleotides a value for at least one parameter that is predictive of the ability of each of said oligonucleotides to hybridize to said target nucleotide sequence and storing said parameter values,

(c) selecting under computer control, from said stored parameter values, a subset of oligonucleotides within said predetermined number of non-identical oligonucleotides based on an examination of said parameter,

(d) identifying under computer control oligonucleotides in said subset that are in clusters along a region of said nucleotide sequence that is hybridizable to said target nucleotide sequence and

(e) under computer control selecting, for a cluster, a hybridization oligonucleotide.

100. **(twice amended)** A computer system for conducting a method for selecting a hybridization oligonucleotide to hybridize to a target nucleotide sequence, said method comprising:

(a) input means for introducing a target nucleotide sequence into said computer system,

(b) means for determining a number of non-identical oligonucleotides that are within a nucleotide sequence that is hybridizable with said target nucleotide sequence, said oligonucleotide sequences being chosen to sample a length of said nucleotide sequence,

(c) memory means for storing said oligonucleotide sequences,

(d) means or controlling said computer system to carry out a determination and evaluation for each of said oligonucleotide sequences a value for at least one